IN THE SPECIFICATION:

At page 23 lines 5-14, please rewrite the paragraph as follows:

As indicated, for some applications, sequence homology (or identity) may be determined using any suitable homology algorithm, using for example default parameters. For a discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.* (1994) Nature Genetics 6:119-129. For some applications, the BLAST algorithm is employed, with parameters set to default values. The BLAST algorithm is described in detail at the NCBI database. Advantageously, "substantial homology", when assessed by BLAST, equates to sequences which match with an EXPECT value of at least about e-7, preferably at least about e-9 and most preferably e-10 or lower. The default threshold for EXPECT in BLAST searching is usually 10.

IN THE CLAIMS:

Please amend Claims 1-2 and 4-6 as follows:

1. (AMENDED) An isolated and/or purified polynucleotide comprising one or more of:

   (a) a polynucleotide encoding a polypeptide comprising SEQ ID NO: 2 or SEQ ID NO: 6;

   (b) a polynucleotide comprising a nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 5;

   (c) a polynucleotide, wherein the complement of said polynucleotide hybridizes to the full length coding sequence of (a) or (b) under moderate stringency;

   (d) a polynucleotide comprising the cDNA of deposit NCIMB 41074; and

   (e) a complement to the polynucleotide of any one of (a), (b), (c), or (d).

2. (AMENDED) The polynucleotide of claim 1, parts (a), (b), or (c), wherein said polynucleotide encodes a G-protein coupled receptor (GPCR).